SEQUENCE COMPARISON


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CC   polypeptide and polynucleotides may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate hTP expression.
CC   The present sequence represents the human transporter protein of the
CC   invention.
XX
SQ   Sequence   465 AA;

  Query Match             100.0%;  Score 2485;  DB 23;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-235;
  Matches  465;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPLKAFLFSPFLLRSQSRGVRLVFLLLTLHLGNCVDKADDEDDEDLTVNKTWVLAPKIH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPLKAFLFSPFLLRSQSRGVRLVFLLLTLHLGNCVDKADDEDDEDLTVNKTWVLAPKIH 60

Qy         61 EGDITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGDITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWF 120

Qy        121 DSRLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWNDGRVLYTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DSRLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWNDGRVLYTL 180

Qy        181 RLTINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLTINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAF 240

Qy        241 VGLRNSTEITHTISGDYVIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VGLRNSTEITHTISGDYVIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVP 300

Qy        301 ARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSN 360

Qy        361 QKGKTATKDRKLKNKASMTPGLHPGSTLIPMNNISVPQEDDYGYQCLEGKDCASFFCCFE 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QKGKTATKDRKLKNKASMTPGLHPGSTLIPMNNISVPQEDDYGYQCLEGKDCASFFCCFE 420

Qy        421 DCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLVYWVGYLYL 465
              |||||||||||||||||||||||||||||||||||||||||||||
Db        421 DCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLVYWVGYLYL 465


RESULT 2
ABB08234
ID   ABB08234 standard; Protein; 465 AA.
XX
AC   ABB08234;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human gamma-amino butyric acid (GABA) receptor subunit #1.
XX
KW   Human; GABA; gamma aminobutyric acid; receptor; gene therapy; protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 257
FT                   /note= "Encoded by TAK"
XX
PN   WO200200720-A2.
XX
PD   03-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-US20417.
XX
PR   27-JUN-2000; 2000US-214083P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW, Friddle CJ, Mathur B, Turner CA;
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102(e)

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XX
DR   WPI; 2002-139905/18.
DR   N-PSDB; ABA96143, ABA96145.
XX
PT   New polynucleotides encoding novel human proteins sharing sequence
PT   similarity with membrane receptors e.g. gamma aminobutyric acid
PT   receptors, for generating primers and probes used to identify drug
PT   targets -
XX
PS   Claim 1; Page 35-37; 38pp; English.
XX
CC   The sequence represents a novel human polypeptide having sequence
CC   similarity with gamma aminobutyric acid (GABA) receptors. The invention
CC   relates to novel human protein (NHP) encoding sequence, where the protein
CC   is a human gamma aminobutyric acid receptor. The sequences may have a use
CC   in gene therapy. The NHP polynucleotide sequences that encode NHPs
CC   sharing sequence similarity with membrane receptors e.g. GABA receptor
CC   subunits, when knocked out provide a method for:
CC   (i) identifying phenotypic expression of the particular gene as well as
CC   assigning function to previously unknown genes,
CC   (ii) identifying a coding sequence and mapping a unique gene to a
CC   particular chromosome; and
CC   (iii) identifying biologically relevant splice junctions.
CC   The NHP polynucleotide sequences are useful:
CC   (i) in gene therapy techniques for the modulation of NHP expression;
CC   (ii) for detecting mutant NHPs or inappropriately expressed NHPs for
CC   the diagnosis of disease;
CC   (iii) for screening drugs effective in treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body.
CC   The sequences are also useful for identifying mutations associated with a
CC   particular disease and also as a prognostic or diagnostic assay. The
CC   nucleic acid molecule is also useful in the molecular mutagenesis/
CC   evolution of proteins that are at least partially encoded by the
CC   described new sequences.
XX
SQ   Sequence   465 AA;

  Query Match             100.0%;  Score 2485;  DB 23;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-235;
  Matches  465;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPLKAFLFSPFLLRSQSRGVRLVFLLLTLHLGNCVDKADDEDDEDLTVNKTWVLAPKIH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPLKAFLFSPFLLRSQSRGVRLVFLLLTLHLGNCVDKADDEDDEDLTVNKTWVLAPKIH 60

Qy         61 EGDITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGDITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWF 120

Qy        121 DSRLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWNDGRVLYTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DSRLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWNDGRVLYTL 180

Qy        181 RLTINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLTINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAF 240

Qy        241 VGLRNSTEITHTISGDYVIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VGLRNSTEITHTISGDYVIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVP 300

Qy        301 ARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSN 360

Qy        361 QKGKTATKDRKLKNKASMTPGLHPGSTLIPMNNISVPQEDDYGYQCLEGKDCASFFCCFE 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QKGKTATKDRKLKNKASMTPGLHPGSTLIPMNNISVPQEDDYGYQCLEGKDCASFFCCFE 420

Qy        421 DCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLVYWVGYLYL 465
              |||||||||||||||||||||||||||||||||||||||||||||
Db        421 DCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLVYWVGYLYL 465
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